

FHF-1	-----MAAAIASSLIRQKQQARESNS-DRVSASKRRSSPSKDG-R	38
FGF-10	-----MAAAIASGLIRQKQQAREQHW-DRPSASRRRSSPSKN--R	37
FHF-4	-----MAAAIASSLIRQKQQAERER---EKSNAACKCVSSPSKG--K	35
FHF-2	-----MAALASSLIRQKREVREPGG-SRPVSAQRRVCP-RGT-K	36
FHF-3	-----MS-GPGTAAVALLPAVLLALL-APWAGRGGAAPTAPN-G	37
FGF4 HUMAN	MALGQKLFITMSRGAGRLQGTLWALVFLGIL-VGMVVP--SPAGTRAN-N	46
FGF6 HUMAN	-----	
FGF2 HUMAN	-----	
FGF1 HUMAN	-----	
KGF-2	-----MWKWILTHCASAFPHLPGCC-CCFLLLFLVSSVPVTC-Q	38
FGF7 HUMAN	-----MHKWILTWILPTLLYR-S-----CFHIICLVGTISLAC-N	33
ZGI HUZFGE	-----MY-SAPSACTCLCLHFLLLCF-QVQ-----VLVAEE-N	30
FGF8 HUMAN	-----MG-SPRSALSCLLLHLLVLCL-QAQEGPGRGPALGREL-A	37
FGF5 HUMAN	-----MSLSFLLLLFFSHLILSAWAHGEKRLAPKGQPGPAATDRN	40
FGF9 HUMAN	-----MAPLGEVGNVYFGVQDAVPFGNVPVLP--VDSPVLLS-D	35
FGF3 HUMAN	-----MGLIWLIIIIISLLEP-----G-----WPAAGPGA	23
FHF-1	SLCERHV---LGVFSKVRFCSGR-----KRPVRRRPEPQLKGIVT	75
FGF-10	-----MASKEPQLKGIVT	13
FHF-4	GLCNGNL---VDIFSKVRIFGLK-----KRRLRRQ-DPQLKGIVT	73
FHF-2	TSCDKNK---LNVFSRVKLFSGK-----KRRRRRP-EPQLKGIVT	71
FHF-3	SLCQKQL---LILLSKVRICGGRP-----ARPDGRP-EPQLKGIVT	73
FGF4 HUMAN	TLEAELERR-WESLVALSLARLPVAAQPK-AAVQSGAGDYLLG-IKRLR	84
FGF6 HUMAN	TLLDS--RG-WGTLLSRSRAGL---AG--E-IAGVNWESGYLVG-IKROR	86
FGF2 HUMAN	-----MAAGSITTLPALPE-----DGGSGAFPPGHFKDPK	30
FGF1 HUMAN	-----MAEGEITTTALTE-----KFN---LPPGNYKKPK	27
KGF-2	ALGQDMVSP-EATNSSSSSFSSPSSAG-----RHVRSYNHLOG-DVRWR	80
FGF7 HUMAN	DMTPEQM---ATNVNCS---SPE-----RHTRSVDYMEGGDIRVR	67
ZGI HUZFGE	VDFRIH-----VEN-----QTRARDDVSRKQLRLY	55
FGF8 HUMAN	SLFRAGR---EPQGVSQHVRE-----QSLVTDQLSRRLIRTY	72
FGF5 HUMAN	PIGSSSRQSSSSAMSSSSASSSPAASLGSQSGLEQSSSQWSPS-GRRTG	89
FGF9 HUMAN	HLGQS-----E--AGGLPRGP-----AVTDLHLKG-ILRRR	64
FGF3 HUMAN	RLRRD-----AGG-----RGGVYEHLGG-APRRR	46
FHF-1	RLFSQQ--GYFLQMHPDGTIDGTDKDNSDYTLFNLIPVGLR-VVAIQGVK	122
FGF-10	RLFSQQ--GYFLQMHPDGTIDGTDKDNSDYTLFNLIPVGLR-VVAIQGVK	60
FHF-4	RLYCRQ--GYFLQMHPDGTIDGTDKDDSTNSTLFNLIPVGLR-VVAIQGVK	120
FHF-2	KLYSRQ--GYHLQLQADGTIDGTDKDEDSTYTLFNLIPVGLR-VVAIQGVQ	118
FHF-3	KLFCRQ--GFYLQANPDGSIQGTPEDTSSFTHFNLIPVGLR-VVTIQSAK	120
FGF4 HUMAN	RLYCNVIGIGFHLQALPDGRIGGAHDT-RDSLLELSPVERG-VVSIFGVA	132
FGF6 HUMAN	RLYCNVIGIGFHLQALPDGRISGTHEEN-PYSLLEISTVERG-VVSLFGVR	134
FGF2 HUMAN	RLYCKNG-GFFLRHPDGRVDGVREKSDPHIKLQLQAEERG-VVSIKGVK	78
FGF1 HUMAN	LLYCSNG-GHFLRILPDGTVDGTRDRSDQHILQLLSAESVG-EVYIKSTE	75
KGF-2	KLFSFT--KYFLKIEKNGKVSCTKENCPSILEITSVEIG-VVAVKAIN	127
FGF7 HUMAN	RLFCRT--QWYLRIDKRGKVKGTQEMKNYNIMEIRTVAVG-IVAIGVE	114
ZGI HUZFGE	QLYSRTS-GKHQVVLG-RRISARGEDGDKYAQLLVETDTFGSQVRIKKE	103
FGF8 HUMAN	QLYSRTS-GKHVQVLANKRINAMAEDGDPFAKLIVETDTFGSRVRVRGAE	121
FGF5 HUMAN	SLYCRVGIGFHLQIYPDGKVNGSHEAN-MLSVLEIFAVSQG-IVGIRGVF	137
FGF9 HUMAN	QLYCRT--GFHLEIFPNGTIQGTGRKDHRSRFGILEFISIAVG-LVSIRGVD	111
FGF3 HUMAN	KLYCAT--KYHLQLHPSGRVNGSLENS-AYSILEITAVEVG-IVAIRGLF	92
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Fig. 1

FHF-1	ASLYVAMNGEGYLYSSDV-FTPECKFKESVFENYYYIYSSSTLYRQQESG-	170
FGF-10	ASLYVAMNGEGYLYSSDV-FTPECKFKESVFENYYYIYSSSTLYRQQESG-	108
FHF-4	TGLYIAMNGEGYLYPSEL-FTPECKFKESVFENYYYIYSSMLYRQQESG-	168
FHF-2	TKLYLAMNSEGYLYTSEL-FTPECKFKESVFENYYVTYSSMIYRQQQSG-	166
FHF-3	LGHYAMNAEGLLYSSPH-FTAECRFKECVFENYYVLYASALYRQRSG-	168
FGF4 HUMAN	SRFFVAMSSKGKLYGSPF-FTDECTFKEILLPNYNAYESYKYPG-----	176
FGF6 HUMAN	SALFVAMNSKGRLYATPS-FQECKFRETLLPNYNAYESDLYQG-----	178
FGF2 HUMAN	ANRYLAMKEDGRLLASKC-VTDECFFERLESNNYNTYRSRKYTS-----	122
FGF1 HUMAN	TGQYLAMDTDGLLYGSQT-PNEECLFLERLEENHYNTYISKKHAEK--N-	121
KGF-2	SNYYLAMNKKGKLYGSKE-FNNDCKLKERIEENGYNTYASFNWQHN--G-	173
FGF7 HUMAN	SEFYLAMNKEGKLYAKKE-CNEDCNFKELILENHYNTYASAKWTHN--G-	160
ZGI FUZFGF	TEFYLCMNRKGKLVGKPDGTSKECVFIEKVLNNYTALMSAKYSG-----	148
FGF8 HUMAN	TGLYICMNNKGKLIASNGKGKDCVFTEIVLENNYTALQNAKYEG-----	166
FGF5 HUMAN	SNKFLAMSKKGKLIHASAK-FTDDCKFRERFQENSYNTYASAIHRTEKTG-	185
FGF9 HUMAN	SGLYLGMNEKGELYGSEK-LTQECVFREQFEENWYNTYSSNLYKHVDTG-	159
FGF3 HUMAN	SGRYLAMNKRGRLYASEH-YSAECEFVERIHELGYNTYASRLYRTVSSTP	141
	:: * . * * . : * : * . *	
FHF-1	-----RAWFLGLNKEGQIMKG--NRVKKTKPSSHFPKPIEVCMYR	209
FGF-10	-----RAWFLGLNKEGQIMKG--NRVEKTKPSSHFPKPIEVCMYR	147
FHF-4	-----RAWFLGLNKEGQAMKG--NRVKKTKPAAHFLPKPLEVAMYR	207
FHF-2	-----RGWYLGLNKEGEIMKG--NHVKKNKPAAHFLPKPLKVAMYK	205
FHF-3	-----RAWYLGLDKEGQVMKG--NRVKKTKAAAHFLPKLLEVAMYQ	207
FGF4 HUMAN	-----MFIALSKNGKTKKG--NRVSPTMKVTHFLPRL-----	206
FGF6 HUMAN	-----TYIALSKYGRVKRG--SKVSPIMTVTHFLPRI-----	208
FGF2 HUMAN	-----WYVALKRTGQYKLG--SKTGPQKAILFLPMSAKS-----	155
FGF1 HUMAN	-----WYVGLKKNKGCKRG--PRTHYGQKAILFLPLPVSSD---	155
KGF-2	-----RQMYVALNGKGAPRRG--QKTRRKNTSAHFLPMVVHS----	208
FGF7 HUMAN	-----GEMFVALNQKGI PVRG--KKTKEQKTAHFLPMAIT-----	194
ZGI FUZFGF	-----WYVGFTKKGRPRKG--PKTRENQQDVHFMKRYPKGQPEL	185
FGF8 HUMAN	-----WYMAFTRKGRPRKG--SKTRQHOREVHFMKRLPRGHHTT	203
FGF5 HUMAN	-----REWYVALNKRKGAKRGCSRVKQHIHSTHFLPRFKQSEQ-P	225
FGF9 HUMAN	-----RRYYVALNKDGTREG--TRTKRHQKFTHFLPRPVPDPKVP	198
FGF3 HUMAN	GARQPSAERLWYVSVNGKGRPRRG--FKTRRTQKSSLFLPRVLDHRDHE	189
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FHF-1	EPSLHEIGEKO----GRS--RKSSGTPTMNGGKVVNQDST-----	243
FGF-10	EPSLHEIGENK----GVQ--GKFWTPP-----	168
FHF-4	EPSLHDVGETVPKP-GVTPSKSTSASAIMNGGKPVNKSCTT-----	247
FHF-2	EPSLHDLTEFSRSG-SGTPTKSRSVSGVLNGGKSMHNEST-----	245
FHF-3	EPSLHSVPEAS-----P--SSPPAP-----	225
FGF4 HUMAN	-----	
FGF6 HUMAN	-----	
FGF2 HUMAN	-----	
FGF1 HUMAN	-----	
KGF-2	-----	
FGF7 HUMAN	-----	
ZGI FUZFGF	QKPFKYTTVTK-----RSRR--IRPHTPA-----	207
FGF8 HUMAN	EQSLRFEFLNYPPF-TRSLRGSRQTWAPEPR-----	233
FGF5 HUMAN	ELSFTVTVPKKNP-PSPIKSKIPLSAPRKNTNSVKYRLKFRFG-----	268
FGF9 HUMAN	ELYKDILSQS-----	208
FGF3 HUMAN	MVRQLQSGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH	239

Fig. 2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	1.00	0.39	0.43	0.29	0.46	0.33	0.36	0.38	0.37	0.41	0.39	0.40	0.42	0.40	0.35	0.38
2		1.00	0.38	0.34	0.41	0.35	0.38	0.33	0.38	0.44	0.39	0.37	0.37	0.39	0.35	0.60
3			1.00	0.31	0.42	0.34	0.33	0.36	0.34	0.38	0.35	0.37	0.41	0.46	0.35	0.35
4				1.00	0.34	0.53	0.26	0.24	0.26	0.31	0.28	0.30	0.30	0.31	0.28	0.32
5					1.00	0.35	0.39	0.43	0.39	0.39	0.43	0.42	0.44	0.43	0.40	0.43
6						1.00	0.33	0.31	0.33	0.31	0.32	0.34	0.34	0.32	0.36	0.36
7							1.00	0.34	0.98	0.33	0.76	0.81	0.34	0.37	0.67	0.42
8								1.00	0.34	0.54	0.34	0.37	0.36	0.36	0.34	0.38
9									1.00	0.33	0.66	0.72	0.34	0.37	0.62	0.42
10										1.00	0.32	0.35	0.40	0.37	0.32	0.43
11											1.00	0.68	0.36	0.38	0.58	0.41
12												1.00	0.36	0.33	0.62	0.42
13													1.00	0.47	0.34	0.32
14														1.00	0.30	0.31
15															1.00	0.38
16																1.00

Fig. 3

	10	20	30	40	50	60
HZFGF5	EENVDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQVLGRRISARGEDGDKYAQLL					
					
MZFGF5	EENVDFRIHVENQTRARDDVSRKQLRLYQLYSRTSGKHIQVLGRRISARGEDGDKYAQLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
HZFGF5	VETDTFGSQVRIKGETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYS					
					
MZFGF5	VETDTFGSQVRIKGETEFYLCMNRKGKLVGKPDGTSKECVFIEKVLENNYTALMSAKYS					
	70	80	90	100	110	120
	130	140	150	160	170	180
HZFGF5	GWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKGQPELQKPFKYTTVTKRSTRIRPHTPA					
					
MZFGF5	GWYVGFTKKGRPRKGPKTRENQQDVHFMKRYPKGQAEELQKPFKYTTVTKRSTRIRPHTPG					
	130	140	150	160	170	180

Fig. 4